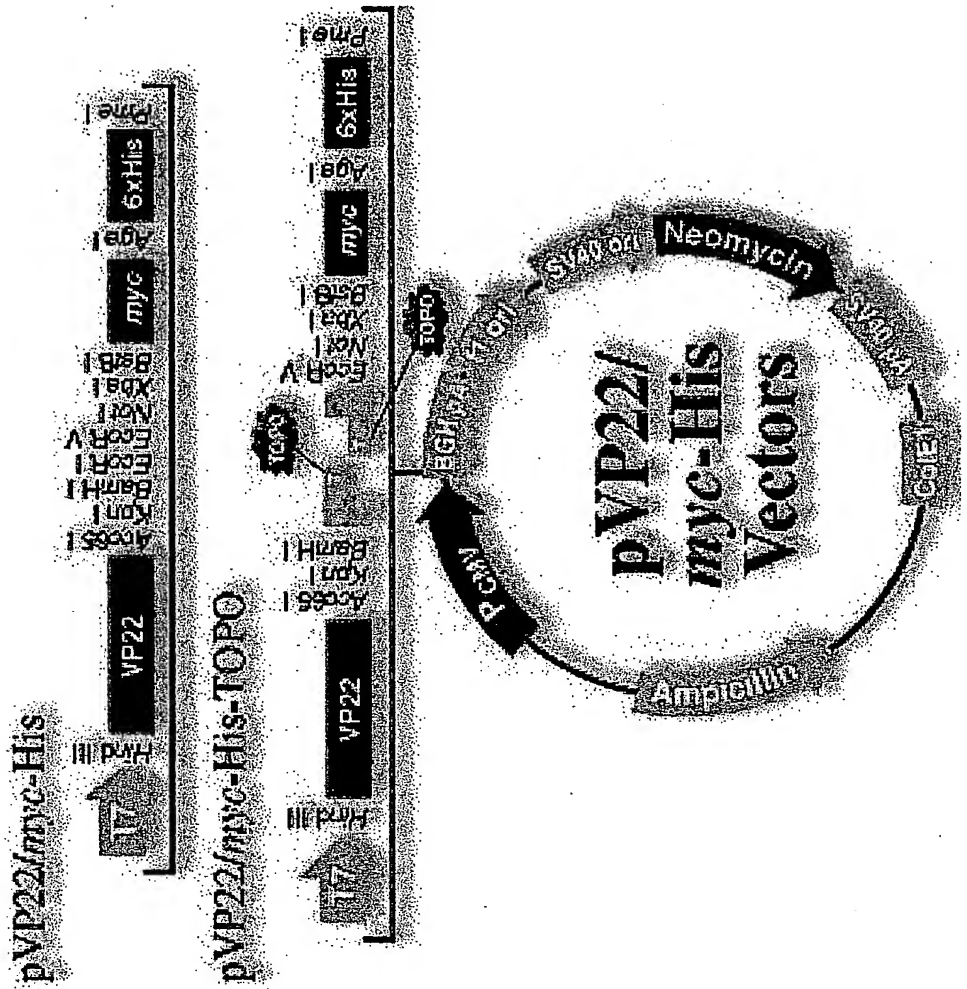


Figure 1

# VP22-REP CONSTRUCTION

AAV2 REP



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Figure 2

# REP-VP22 CONSTRUCTION

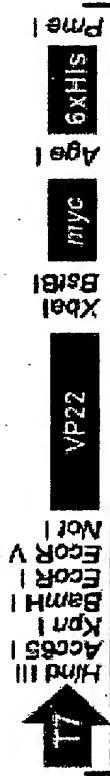
AAV2 REP



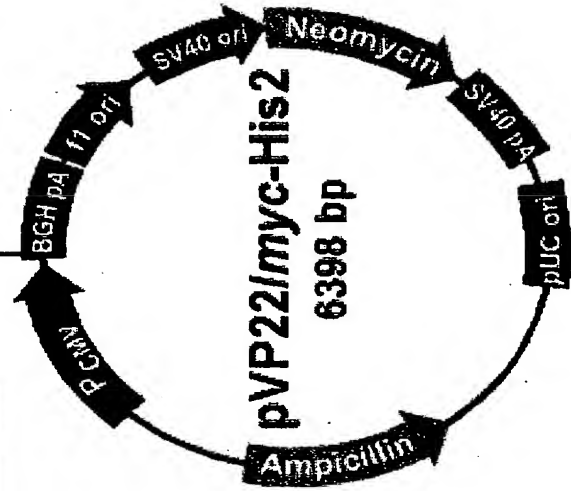
Not I

EcoRV

1. STOP->CYS
2. PHE->CYS
- LAST 2 AA DROPPED



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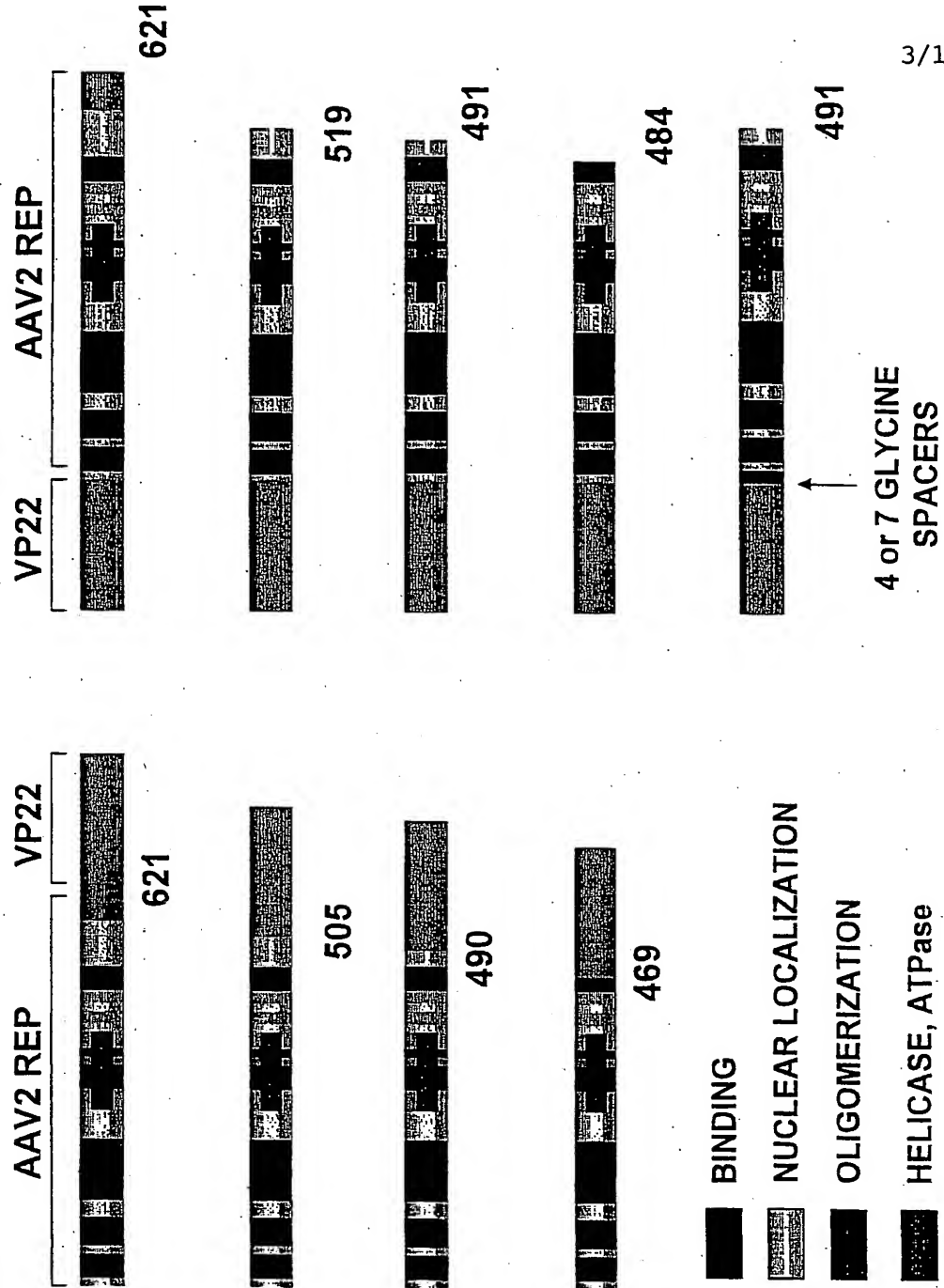


Figure 3A

Figure 3B

## WESTERN ANALYSIS OF REP<sub>490</sub>-VP22 EXPRESSION

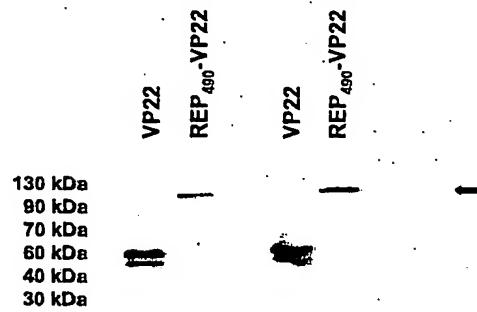
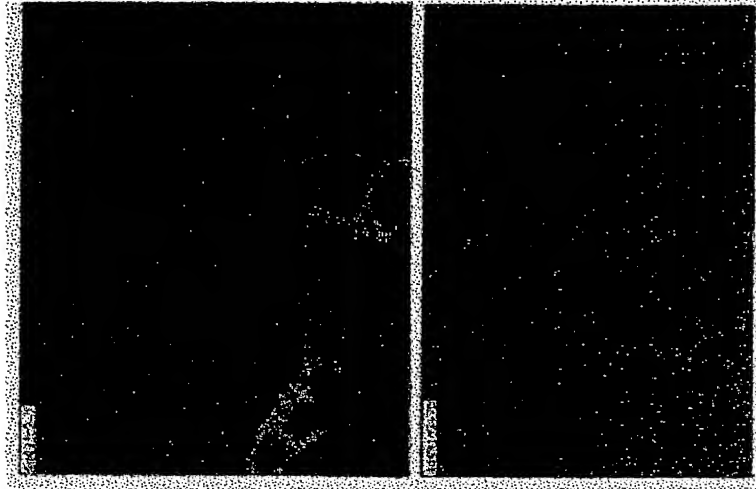


Figure 4

VP4glyRep491



VPRep491

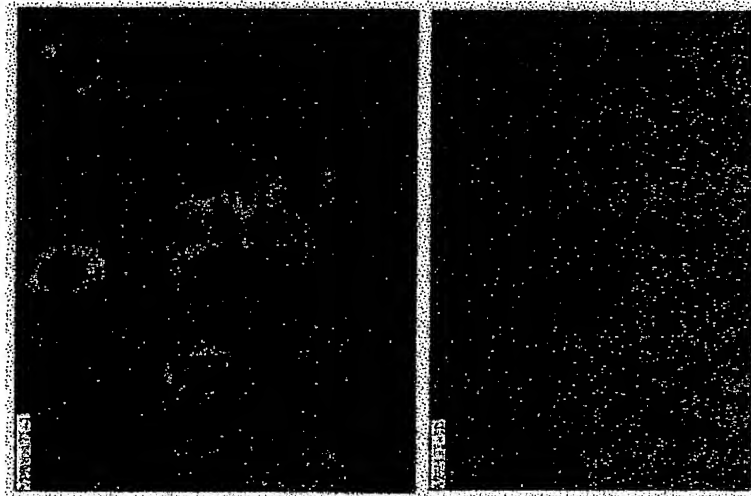
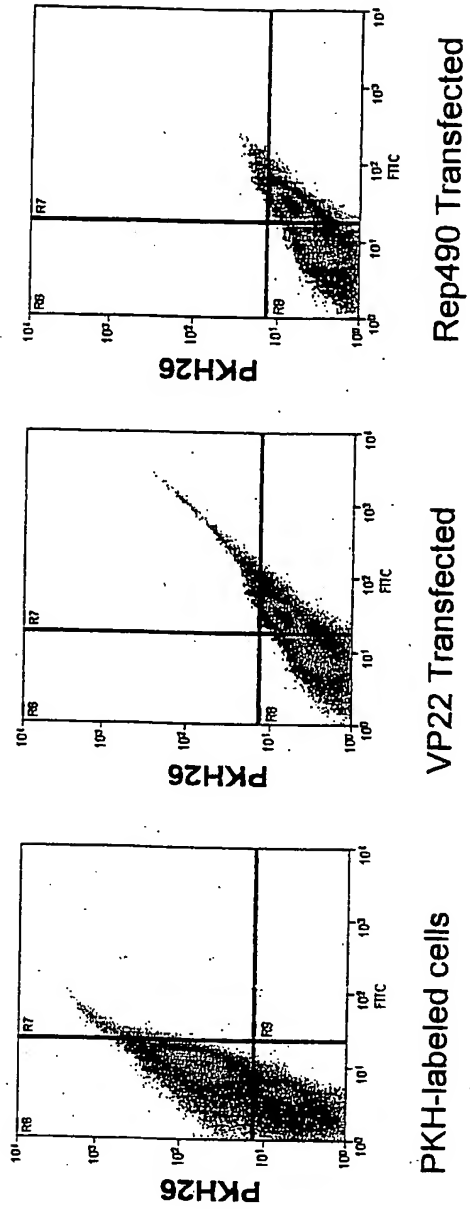


Figure 5

BEST AVAILABLE COPY



SINGLE POPULATIONS



MIXED POPULATIONS

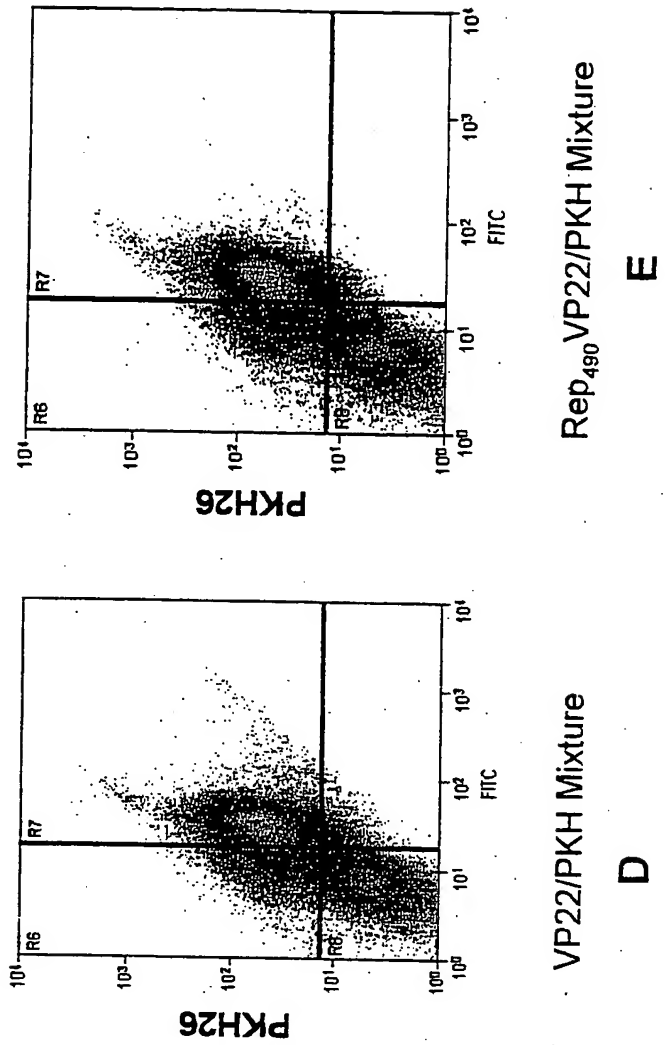


Figure 7

BEST AVAILABLE COPY

Figure 8A

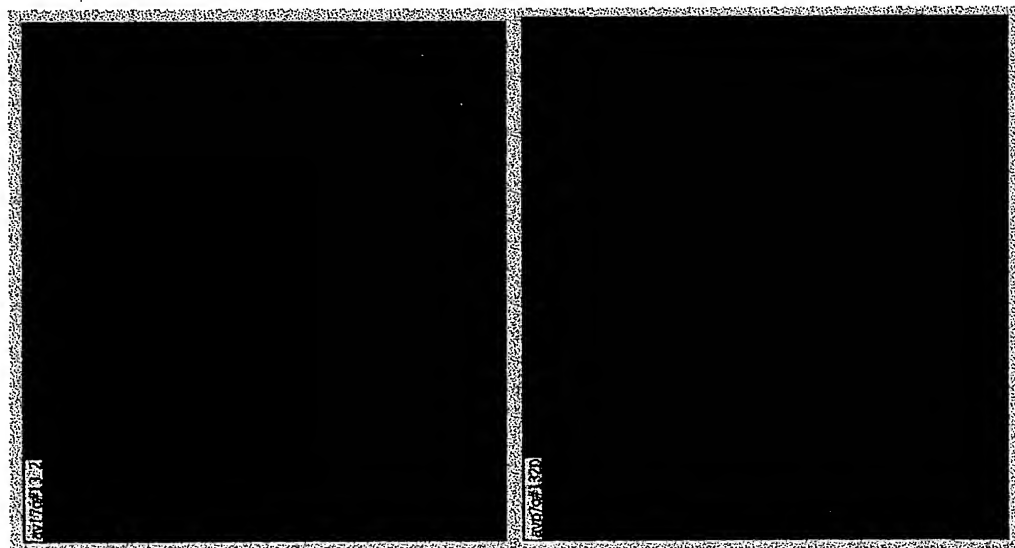


Figure 8B

AAVS1 Probe

M 1 2 3 4 5 6

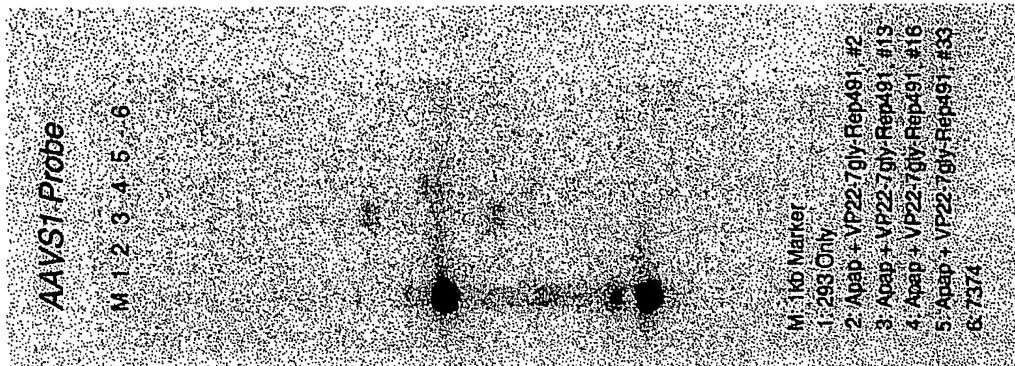


Figure 10

AAV Probe

M 1 2 3 4 5 6

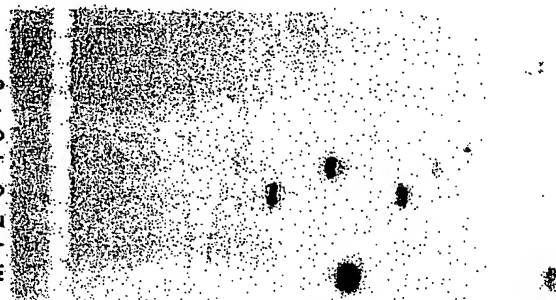


Figure 9

M: 1 kb Marker

- 1: 293 Only
- 2: Aap + VP22-7gly-Rep491, #2
- 3: Aap + VP22-7gly-Rep491, #13
- 4: Aap + VP22-7gly-Rep491, #16
- 5: Aap + VP22-7gly-Rep491, #33
- 6: 7374

M: 1 kb Marker

- 1: 293 Only
- 2: Aap + VP22-7gly-Rep491, #2
- 3: Aap + VP22-7gly-Rep491, #13
- 4: Aap + VP22-7gly-Rep491, #16
- 5: Aap + VP22-7gly-Rep491, #33
- 6: 7374



**rAAV-CELL JUNCTION SEQUENCE  
ANALYSIS VP22<sub>4GLY</sub>REP<sub>491</sub>**

>gi|341631|gb|M27086.1|HUMAAV02 Homo sapiens DNA fragment containing the 3'  
adeno-associated virus/cellular junction Length = 875 Score = 686 bits (346),  
Expect = 0.0 Identities = 393/402 (97%), Gaps = 5/402 (1%) Strand = Plus / Plus.

```

Query:   101      taacaggacatccotaa-ccctatgacgtaattoacgtaacgactcattccotgacccgccc 159
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Sbjct:   362      taacaggacatccotaaatccctatgacgtaattoacgtaacgactcattccotgacccgccc 421
Query:   160      ctctccctgaacccctgagccagctcccatagctcagctctggtctatctgacccggccctggcc 219
          |||
Sbjct:   422      ctctccctgaacccctgagccagctcccatagctcagctctggtctatctgacccggccctggcc- 480
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Sbjct:   481      attgtaactttgagctgcccctcctctcgcgcgcgcgagtgcccttgctgtgcgcgcgggaact 539
Query:   280      ctgccctctataacgctgcgctctctctcctgagtcaggacaaactttgagctctactggctt 339
          |||
Sbjct:   540      ctgccctctataacgctgcgctctctctcctgagtcaggacaaactttgagctctactggctt 599

```

Figure 11

